

SEQUENCE LISTING

<110> Allison, Anthony  
<120> MODIFIED ANNEXIN PROTEINS AND METHODS FOR TREATING VASO-OCCLUSIVE SICKLE-CELL DISEASE  
<130> SURR.113  
<150> 60/400,718  
<151> 2002-08-02  
<150> 10/080,370  
<151> 2002-02-21  
<160> 9  
<170> PatentIn version 3.2  
<210> 1  
<211> 960  
<212> DNA  
<213> Homo sapiens  
<400> 1  
atggccctgc gcggcaccgt gaccgacttc tccggcttcg acggccgcgc cgacgcccag 60  
gtgctgcgca aggccatgaa gggcctgggc accgacgagg actccatcct gaacctgctg 120  
accgccccgt ccaacgcccga gcgccagcag atcgccgagg agttcaagac cctgttcggc 180  
cgcgacctgg tgaacgacat gaagtccgag ctgaccggca agttcgagaa gctgatcgtg 240  
gccctgatga agccctcccg cctgtacgac gcctacgagc tgaagcacgc caagctggc 300  
gccggcaccg acgagaaggt gctgaccgag atcatcgccct cccgcacccc cgaggagctg 360  
cgcgccatca agcaggccta cgaggaggag tacggctcca acctggagga cgacgtggtg 420  
ggcgacacccct ccggctacta ccagcgcattt ctgggtgtc tgctgcaggc caaccgcgac 480  
cccgacacccg ccatcgacga cgcccaggtg gagctggacg cccaggccct gttccaggcc 540  
ggcgagctga agtgggcac cgacgaggag aagttcatca ccatcctggg caccgcgtcc 600  
gtgtcccacc tgcggcgcgt gttcgacaag tacatgacca tctccggctt ccagatcgag 660  
gagaccatcg accgcgagac ctccggcaac ctggagaacc tgctgctggc cgtggtaag 720  
tccatccgctt ccatccccgc ctacctggcc gagaccctgt actacgcccattt gaagggcgcc 780  
ggcacccgacg accacacccct gatccgcgtg atcgtgtccc gctccgagat cgacctgttc 840  
aacatccgca aggagttccg caagaacttc gccacccctt tgcactccat gatcaaggc 900

gacacacctccg gcgactacaa gaaggccctg ctgctgctgt gcggcggcga ggacgactga 960  
  
 <210> 2  
 <211> 960  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> (1)..(960)  
  
 <400> 2  
 atg gcc ctg cgc ggc acc gtg acc gac ttc tcc ggc ttc gac ggc cgc 48  
 Met Ala Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg  
 1 5 10 15  
  
 gcc gac gcc gag gtg ctg cgc aag gcc atg aag ggc ctg ggc acc gac 96  
 Ala Asp Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp  
 20 25 30  
  
 gag gac tcc atc ctg aac ctg ctg acc gcc cgc tcc aac gcc cag cgc 144  
 Glu Asp Ser Ile Leu Asn Leu Thr Ala Arg Ser Asn Ala Gln Arg  
 35 40 45  
  
 cag cag atc gcc gag gag ttc aag acc ctg ttc ggc cgc gac ctg gtg 192  
 Gln Gln Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val  
 50 55 60  
  
 aac gac atg aag tcc gag ctg acc ggc aag ttc gag aag ctg atc gtg 240  
 Asn Asp Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val  
 65 70 75 80  
  
 gcc ctg atg aag ccc tcc cgc ctg tac gac gcc tac gag ctg aag cac 288  
 Ala Leu Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His  
 85 90 95  
  
 gcc aag ctg ggc gcc ggc acc gac gag aag gtg ctg acc gag atc atc 336  
 Ala Lys Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile  
 100 105 110  
  
 gcc tcc cgc acc ccc gag gag ctg cgc gcc atc aag cag gcc tac gag 384  
 Ala Ser Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu  
 115 120 125  
  
 gag gag tac ggc tcc aac ctg gag gac gac gtg gtg ggc gac acc tcc 432  
 Glu Glu Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser  
 130 135 140  
  
 ggc tac tac cag cgc atg ctg gtg gtg ctg cag gcc aac cgc gac 480  
 Gly Tyr Tyr Gln Arg Met Leu Val Val Leu Gln Ala Asn Arg Asp  
 145 150 155 160  
  
 ccc gac acc gcc atc gac gac gcc cag gtg gag ctg gac gcc cag gcc 528  
 Pro Asp Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala

165	170	175	
ctg ttc cag gcc ggc gag ctg aag tgg ggc acc gac gag gag aag ttc Leu Phe Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe 180	185	190	576
atc acc atc ctg ggc acc cgc tcc gtg tcc cac ctg cgc cgc gtg ttc Ile Thr Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe 195	200	205	624
gac aag tac atg acc atc tcc ggc ttc cag atc gag gag acc atc gac Asp Lys Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp 210	215	220	672
cgc gag acc tcc ggc aac ctg gag aac ctg ctg gcc gtg gtg aag Arg Glu Thr Ser Gly Asn Leu Glu Asn Leu Leu Ala Val Val Lys 225	230	235	720
tcc atc cgc tcc atc ccc gcc tac ctg gcc gag acc ctg tac tac gcc Ser Ile Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala 245	250	255	768
atg aag ggc gcc ggc acc gac gac cac acc ctg atc cgc gtg atc gtg Met Lys Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val 260	265	270	816
tcc cgc tcc gag atc gac ctg ttc aac atc cgc aag gag ttc cgc aag Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys 275	280	285	864
aac ttc gcc acc tcc ctg tac tcc atg atc aag ggc gac acc tcc ggc Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly 290	295	300	912
gac tac aag aag gcc ctg ctg ctg tgc ggc ggc gag gac gac tga Asp Tyr Lys Lys Ala Leu Leu Leu Cys Gly Gly Glu Asp Asp 305	310	315	960
<210> 3			
<211> 319			
<212> PRT			
<213> Homo sapiens			
<400> 3			
Met Ala Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg 1	5	10	15
Ala Asp Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp 20	25	30	
Glu Asp Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg 35	40	45	

Gln Gln Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val  
50 55 60

Asn Asp Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val  
65 70 75 80

Ala Leu Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His  
85 90 95

Ala Lys Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile  
100 105 110

Ala Ser Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu  
115 120 125

Glu Glu Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser  
130 135 140

Gly Tyr Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp  
145 150 155 160

Pro Asp Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala  
165 170 175

Leu Phe Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe  
180 185 190

Ile Thr Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe  
195 200 205

Asp Lys Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp  
210 215 220

Arg Glu Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys  
225 230 235 240

Ser Ile Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala  
245 250 255

Met Lys Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val  
260 265 270

Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys  
275 280 285

Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly  
290 295 300

Asp Tyr Lys Lys Ala Leu Leu Leu Cys Gly Gly Glu Asp Asp  
305 310 315

<210> 4  
<211> 2016  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<220>  
<221> misc\_feature  
<222> (45)..(45)  
<223> n = a, c, t, or g

<220>  
<221> misc\_feature  
<222> (1000)..(1002)  
<223> n = a, c, t, or g

<220>  
<221> misc\_feature  
<222> (1051)..(1053)  
<223> n = a, c, t, or g

<400> 4  
atggactaca aagacgatga cgacaagctt gcggccgcga attcngccct gcgccggacc 60  
gtgaccgact tctccggctt cgacggccgc gccgacgccc aggtgctgcg caaggccatg 120  
aagggcctgg gcacccgacga ggactccatc ctgaacctgc tgaccgcccc ctccaacgcc 180  
cagcgccagc agatcgccga ggagttcaag accctgttcg gccgcgacct ggtgaacgac 240  
atgaagtccg agctgaccgg caagttcgag aagctgatcg tggccctgat gaagccctcc 300  
cgccctgtacg acgcctacga gctgaagcac gccaagctgg gcgccggcac cgacgagaag 360  
gtgctgaccg agatcatcgc ctcccgccacc cccgaggagc tgcgccat caagcaggcc 420  
tacgaggagg agtacggctc caacctggag gacgacgtgg tgggcgacac ctccggctac 480  
taccagcgca tgctgggtggt gctgctgcag gccaaccgcg accccgacac cgccatcgac 540  
gacgcccagg tggagctgga cgcccaggcc ctgttccagg ccggcgagct gaagtggggc 600

accgacgagg	agaagttcat	caccatcctg	ggcacccgct	ccgtgtccca	cctgcgccgc	660
gtgttcgaca	agtacatgac	catctccggc	ttccagatcg	aggagaccat	cgaccgcgag	720
acctccggca	acctggagaa	cctgctgctg	gccgtggta	agtccatccg	ctccatcccc	780
gcctacctgg	ccgagaccct	gtactacgcc	atgaagggcg	ccggcaccga	cgaccacacc	840
ctgatccgcg	tgatcggtc	ccgctccgag	atcgacctgt	tcaacatccg	caaggagttc	900
cgcaagaact	tcgcccaccc	cctgtactcc	atgatcaagg	gcgacaccc	cgccgactac	960
aagaaggccc	tgctgctgct	gtgcggcggc	gaggacgacn	nnagatctcg	atcgggcctg	1020
gaggtgctgt	tccagggccc	cggaagtact	nnngccctgc	gcccgcaccgt	gaccgacttc	1080
tccggcttcg	acggccgcgc	cgacgccgag	gtgctgcga	aggccatgaa	gggcctggc	1140
accgacgagg	actccatcct	gaacctgctg	accgcccgt	ccaacgccc	gcgcacagcag	1200
atcgccgagg	agttcaagac	cctgttcggc	cgcgacctgg	tgaacgacat	gaagtccgag	1260
ctgaccggca	agttcgagaa	gctgatcggt	gccctgatga	agccctcccg	cctgtacgac	1320
gcctacgagc	tgaagcacgc	caagctggc	gccggcaccg	acgagaaggt	gctgaccgag	1380
atcatcgccct	cccgccaccc	cgaggagctg	cgccatca	agcaggccta	cgaggaggag	1440
tacggctcca	acctggagga	cgacgtggtg	ggcgacacct	ccggctacta	ccagcgcatt	1500
ctgggtgtgc	tgctgcagggc	caaccgcgac	cccgacaccg	ccatcgacga	cgcccaggtg	1560
gagctggacg	cccaggccct	gttccaggcc	ggcgagctga	agtggggcac	cgacgaggag	1620
aagttcatca	ccatcctggg	cacccgctcc	gtgtcccacc	tgcggcgct	gttcgacaag	1680
tacatgacca	tctccggctt	ccagatcgag	gagaccatcg	accgcgagac	ctccggcaac	1740
ctggagaacc	tgctgctggc	cgtggtgaag	tccatccgt	ccatccccgc	ctacccggcc	1800
gagaccctgt	actacgccc	gaagggcgcc	ggcacccgacg	accacaccct	gatccgcgtg	1860
atcggttccc	gttccgagat	cgacctgttc	aacatccgca	aggagttccg	caagaacttc	1920
gccacccccc	tgtactccat	gatcaagggc	gacaccctcg	gcgactacaa	gaaggccctg	1980
ctgctgctgt	gcggcggcga	ggacgactaa	taataa		2016	

<210> 5  
 <211> 2016  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

```

<220>
<221> CDS
<222> (1)..(2016)

<220>
<221> misc_feature
<222> (45)..(45)
<223> n = a, c, t, or g

<220>
<221> misc_feature
<222> (1000)..(1002)
<223> n = a, c, t, or g

<220>
<221> misc_feature
<222> (1051)..(1053)
<223> n = a, c, t, or g

<400> 5
atg gac tac aaa gac gat gac gac aag ctt gcg gcc gcg aat tcn gcc      48
Met Asp Tyr Lys Asp Asp Asp Asp Lys Leu Ala Ala Ala Asn Xaa Ala
1           5           10          15

ctg cgc ggc acc gtg acc gac ttc tcc ggc ttc gac ggc cgc gcc gac      96
Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp
20          25          30

gcc gag gtg ctg cgc aag gcc atg aag ggc ctg ggc acc gac gag gac      144
Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp
35          40          45

tcc atc ctg aac ctg ctg acc gcc cgc tcc aac gcc cag cgc cag cag      192
Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln
50          55          60

atc gcc gag gag ttc aag acc ctg ttc ggc cgc gac ctg gtg aac gac      240
Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp
65          70          75          80

atg aag tcc gag ctg acc ggc aag ttc gag aag ctg atc gtg gcc ctg      288
Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu
85          90          95

atg aag ccc tcc cgc ctg tac gac gcc tac gag ctg aag cac gcc aag      336
Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Lys
100         105         110

ctg ggc gcc ggc acc gac gag aag gtg ctg acc gag atc atc gcc tcc      384
Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser
115         120         125

cgc acc ccc gag gag ctg cgc gcc atc aag cag gcc tac gag gag gag      432
Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu Glu Glu
130         135         140

```

tac ggc tcc aac ctg gag gac gac gtg gtg ggc gac acc tcc ggc tac Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr 145 150 155 160	480
tac cag cgc atg ctg gtg ctg ctg cag gcc aac cgc gac ccc gac Tyr Gln Arg Met Leu Val Val Leu Gln Ala Asn Arg Asp Pro Asp 165 170 175	528
acc gcc atc gac gac gcc cag gtg gag ctg gac gcc cag gcc ctg ttc Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe 180 185 190	576
cag gcc ggc gag ctg aag tgg ggc acc gac gag gag aag ttc atc acc Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr 195 200 205	624
atc ctg ggc acc cgc tcc gtg tcc cac ctg cgc cgc gtg ttc gac aag Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys 210 215 220	672
tac atg acc atc tcc ggc ttc cag atc gag gag acc atc gac cgc gag Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu 225 230 235 240	720
acc tcc ggc aac ctg gag aac ctg ctg gcc gtg gtg aag tcc atc Thr Ser Gly Asn Leu Glu Asn Leu Leu Ala Val Val Lys Ser Ile 245 250 255	768
cgc tcc atc ccc gcc tac ctg gcc gag acc ctg tac tac gcc atg aag Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys 260 265 270	816
ggc gcc ggc acc gac gac cac acc ctg atc cgc gtg atc gtg tcc cgc Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg 275 280 285	864
tcc gag atc gac ctg ttc aac atc cgc aag gag ttc cgc aag aac ttc Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe 290 295 300	912
gcc acc tcc ctg tac tcc atg atc aag ggc gac acc tcc ggc gac tac Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr 305 310 315 320	960
aag aag gcc ctg ctg ctg tgc ggc ggc gag gac gac nnn aga tct Lys Lys Ala Leu Leu Leu Cys Gly Gly Glu Asp Asp Xaa Arg Ser 325 330 335	1008
cga tcg ggc ctg gag gtg ctg ttc cag ggc ccc gga agt act nnn gcc Arg Ser Gly Leu Glu Val Leu Phe Gln Gly Pro Gly Ser Thr Xaa Ala 340 345 350	1056
ctg cgc ggc acc gtg acc gac ttc tcc ggc ttc gac ggc cgc gcc gac Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp 355 360 365	1104
gcc gag gtg ctg cgc aag gcc atg aag ggc ctg ggc acc gac gag gac	1152

Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp			
370	375	380	
tcc atc ctg aac ctg ctg acc gcc cgc tcc aac gcc cag cgc cag cag			1200
Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln			
385	390	395	400
atc gcc gag gag ttc aag acc ctg ttc ggc cgc gac ctg gtg aac gac			1248
Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp			
405	410	415	
atg aag tcc gag ctg acc ggc aag ttc gag aag ctg atc gtg gcc ctg			1296
Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu			
420	425	430	
atg aag ccc tcc cgc ctg tac gac gcc tac gag ctg aag cac gcc aag			1344
Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Lys			
435	440	445	
ctg ggc gcc ggc acc gac gag aag gtg ctg acc gag atc atc gcc tcc			1392
Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser			
450	455	460	
cgc acc ccc gag gag ctg cgc gcc atc aag cag gcc tac gag gag gag			1440
Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu Glu Glu			
465	470	475	480
tac ggc tcc aac ctg gag gac gtg gtg ggc gac acc tcc ggc tac			1488
Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr			
485	490	495	
tac cag cgc atg ctg gtg ctg ctg cag gcc aac cgc gac ccc gac			1536
Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp			
500	505	510	
acc gcc atc gac gac gcc cag gtg gag ctg gac gcc cag gcc ctg ttc			1584
Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe			
515	520	525	
cag gcc ggc gag ctg aag tgg ggc acc gac gag gag aag ttc atc acc			1632
Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr			
530	535	540	
atc ctg ggc acc cgc tcc gtg tcc cac ctg cgc cgc gtg ttc gac aag			1680
Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys			
545	550	555	560
tac atg acc atc tcc ggc ttc cag atc gag gag acc atc gac cgc gag			1728
Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu			
565	570	575	
acc tcc ggc aac ctg gag aac ctg ctg gcc gtg gtg aag tcc atc			1776
Thr Ser Gly Asn Leu Glu Asn Leu Leu Ala Val Val Lys Ser Ile			
580	585	590	
cgc tcc atc ccc gcc tac ctg gcc gag acc ctg tac tac gcc atg aag			1824
Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys			

595

600

605

ggc gcc ggc acc gac gac cac acc ctg atc cgc gtg atc gtg tcc cgc	1872
Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg	
610 615 620	
tcc gag atc gac ctg ttc aac atc cgc aag gag ttc cgc aag aac ttc	1920
Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe	
625 630 635 640	
gcc acc tcc ctg tac tcc atg atc aag ggc gac acc tcc ggc gac tac	1968
Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr	
645 650 655	
aag aag gcc ctg ctg ctg tgc ggc ggc gag gac gac taa taa taa	2016
Lys Lys Ala Leu Leu Leu Cys Gly Gly Glu Asp Asp	
660 665	

<210> 6  
<211> 669  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (15)..(15)  
<223> The 'Xaa' at location 15 stands for Ser.

<220>  
<221> misc\_feature  
<222> (334)..(334)  
<223> The 'Xaa' at location 334 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (351)..(351)  
<223> The 'Xaa' at location 351 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

<220>  
<223> primer

<400> 6

Met Asp Tyr Lys Asp Asp Asp Asp Lys Leu Ala Ala Ala Asn Xaa Ala  
1 5 10 15

Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp  
20 25 30

Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp

35

40

45

Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln  
50 55 60

Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp  
65 70 75 80

Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu  
85 90 95

Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Lys  
100 105 110

Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser  
115 120 125

Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu Glu Glu  
130 135 140

Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr  
145 150 155 160

Tyr Gln Arg Met Leu Val Val Leu Gln Ala Asn Arg Asp Pro Asp  
165 170 175

Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe  
180 185 190

Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr  
195 200 205

Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys  
210 215 220

Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu  
225 230 235 240

Thr Ser Gly Asn Leu Glu Asn Leu Leu Ala Val Val Lys Ser Ile  
245 250 255

Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys  
260 265 270

Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg  
275 280 285

Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe  
290 295 300

Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr  
305 310 315 320

Lys Lys Ala Leu Leu Leu Cys Gly Gly Glu Asp Asp Xaa Arg Ser  
325 330 335

Arg Ser Gly Leu Glu Val Leu Phe Gln Gly Pro Gly Ser Thr Xaa Ala  
340 345 350

Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp  
355 360 365

Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp  
370 375 380

Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln  
385 390 395 400

Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp  
405 410 415

Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu  
420 425 430

Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Lys  
435 440 445

Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser  
450 455 460

Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu Glu Glu  
465 470 475 480

Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr  
485 490 495

Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp  
500 505 510

Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe  
515 520 525

Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr  
530 535 540

Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys  
545 550 555 560

Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu  
565 570 575

Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys Ser Ile  
580 585 590

Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys  
595 600 605

Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg  
610 615 620

Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe  
625 630 635 640

Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr  
645 650 655

Lys Lys Ala Leu Leu Leu Cys Gly Gly Glu Asp Asp  
660 665

<210> 7  
<211> 30  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer

<220>  
<221> misc\_feature  
<222> (1)..(30)

<223> primer  
<400> 7  
acctgagtag tcgccatggc acaggttctc 30

<210> 8  
<211> 36  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer  
<400> 8  
cccgaaattca cgtagtcat cttctccaca gagcag 36  
~~~~~  
<210> 9  
<211> 8  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic fusion peptide  
<400> 9  
  
Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

3

S:\CLIENT FOLDERS\SURROMED\113\SEQ LISTING.TXT